

Fig. 1

Target 5'---3' (SEQ ID NO:)	Binding-helix amino acids at positions -1 1 2 3 4 5 6	Specificity
GAA (1)	Q S S N L V R	GAA (GAT)
(17)	Q R S N L V R	GAA, GAT
(18)	Q S G N L V R	GAN
(19)	Q P G N L V R	GAN
GAC (2)	D P G N L V R	GAC
(20)	D P G N L K R	GAC, GAT
GAG (3)	R S D N L V R	GAG
(21)	R S D N L R R	GAG, GGG
(22)	K S A N L V R	GAG, (GAT)
(23)	R S D N L V K	GAG, (GGG)
(24)	K S A Q L V R	UNSPEC.
GAT (4)	T S G N L V R	GAT
GCA (5)	Q S G D L R R	GCA, GCT
(25)	Q S S T L V R	GTA, GCA
(26)	Q S G T L R R	GTA, GCA/T/C
(27)	Q P G D L V R	GCT, GCC, GCA

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	(28)	Q G P D L V R	GCT, GCA
	(29)	Q A G T L M R	GTA, GCA
	(30)	Q P G T L V R	GTA, GCA
	(31)	Q G P E L V R	non-binder
GCC	(6)	D C R D L A R	GCC
	(32)	G C R E L S R	GCC
	(33)	D P S T L K R	GCC (GCA/T GTC)
	(34)	D P S D L K R	GCC, GAC
	(35)	D S G D L V R	GCC, GAC
	(36)	D S G E L V R	GCT, GCC
	(37)	D S G E L K R	GCT, GCC, GTC
GCG	(7)	R S D D L V K	GCG
	(38)	R L D T L G R	GNG
	(39)	R P G D L V R	GCG, GNG, GCN
	(40)	R S D T L V R	NG
	(41)	K S A D L K R	GAG, GTG, GCT, GCC
	(42)	R S D D L V R	GAG, (GNG, GCN)
	(43)	R S D T L V K	GNG

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	(44)	K S A E L K R	GCT, GCC, UNSPEC.
	(45)	K S A E L V R	GCT, GCC, UNSPEC.
	(46)	R G P E L V R	UNSPEC.
	(47)	K P G E L V R	NON-BINDER, BUT EXPR.
GCT	(8)	T S G E L V R	GCT
	(48)	S S Q T L T R	GCT
	(49)	T P G E L V R	GCT
	(50)	T S G D L V R	GCT, (GCC, GCA)
	(51)	S S Q T L V R	GCT
	(52)	T S Q T L T R	GCT (GAT, GTC, GCC)
	(53)	T S G E L K R	GCT, GCC
	(54)	Q S S D L V R	GCT (GCA, GCC)
	(55)	S S G T L V R	GCC, GCT
	(56)	T P G T L V R	GCT, GTC
	(57)	T S Q D L K R	GCC, GCT
	(58)	T S G T L V R	GCT, UNSPEC.
GGA	(9)	Q R A H L E R	GGA
	(59)	Q S S H L V R	GGA
	(60)	Q S G H L V R	GGA

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	(61)	Q P G H L V R	GGA, GCT
GGC	(10)	D P G H L V R	GGC
	(62)	E R S K L A R	GGC
	(63)	D P G H L A R	GGC
	(64)	Q R A K L E R	GGC
	(65)	Q S S K L V R	GGC
	(66)	D R S K L A R	GGC, GGN
	(67)	D P G K L A R	GGC, unspec.
GGG	(11)	R S D K L V R	GGG
	(68)	R S D K L T R	GGG
	(69)	R S D H L T R	GGG, GAG
	(70)	K S A K L E R	NON-BINDER
GGT	(12)	T S G H L V R	GGT, GCA
	(71)	T A D H L S R	GGT, GAT
	(72)	T A D K L S R	GGG, (GGT)
	(73)	T P G H L V R	GGT, unspec.
	(74)	T S S H L V R	unspec.
	(75)	T S G K L V R	unspec.
GTA	(13)	Q S S S L V R	
	(76)	Q P G E L V R	GTA, (GCT)
	(77)	Q S G E L V R	GTA, GCA/C

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	(78)	Q S G E L R R	GTA, GCA/T/C
GTC	(14)	D P G A L V R	
	(79)	D P G S L V R	GTC (GCT, GCC)
GTC	(15)	R S D E L V R	GTG, (GAG, GCG)
	(80)	R K D S L V R	GTG, GNG
	(81)	R S D V L V R	GTG, GAG, GGG
	(82)	R H D S L L R	GTG, GAG, GNG
	(83)	R S D A L V R	GAG, GTG, GGG
	(84)	R S S S L V R	GTG
	(85)	R S S S H V R	GTG, GGG
	(86)	R S D E L V K	GTG
	(87)	R S D A L V K	GAG GTG GGG
	(88)	R S D V L V K	GAG GNG
	(89)	R S S A L V R	GNG
	(90)	R K D S L V K	GGG GNG
	(91)	R S A S L V R	GAG, unsec.
	(92)	R S D S L V R	GCT unsec.
	(93)	R I H S L V R	unsec.

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	(94)	R P G S L V R	UNSPEC.
	(95)	R G P S L V R	UNSPEC.
	(96)	R P G A L V R	UNSPEC.
	(97)	K S A S L V R	NON-BINDER
	(98)	K S A A L V R	NON-BINDER
	(99)	K S A V L V R	NON-BINDER
GTT	(16)	T S G S L V R	GTT, GCT
	(100)	T S G S L T R	GGT, GCT
	(101)	T S Q S L V R	GAT, GTA GCT, GCA
	(102)	T S S S L V R	GTA, GAT
	(103)	T P G S L V R	GTA
	(104)	T S G A L V R	GGT, GCT, GAT
	(105)	T P G A L V R	GGT, GAT, GCT
	(106)	T G G S L V R	GGT, GAT
	(107)	T S G E L V R	GCT GCG GTA GTT
	(108)	T S G E L T R	GCT GTA/T/C
	(109)	T S S A L V K	UNSPEC
	(110)	T S S A L V R	UNSPEC

A

-30	erbB-2	-1	
AGCCATGGGGCCGGAGCCGCAGTGAGCACC			SEQ ID NO: 123
GCAATCGGAGCCGGAGCCGGAGTCCGGGGA			SEQ ID NO: 124
-135	erbB-3	-164	

B

	10	20	30	40	
E2C	MAQAAL	EPGEKPYACPECGKSFS	SRKDSLVR	HQRTHTGEKP	
E3	MAQAAL	EPGEKPYACPECGKSFS	SDPGALVR	HQRTHTGEKP	
	50	60	70	80	
E2C	YKCPECGKSFS	QSGDLRRH	HQRTHTGEKPYKCPECGKSFS	SD	
E3	YKCPECGKSFS	QSSHLVR	HQRTHTGEKPYKCPECGKSFS	SD	
	90	100	110	120	
E2C	CRDLAR	HQRTHTGEKPYACPECGKSFS	QSSHLVR	HQRTHT	
E3	CRDLAR	HQRTHTGEKPYACPECGKSFS	QSSHLVR	HQRTHT	
	130	140	150	160	
E2C	GEKPYKCPECGKSFS	SDCRDLAR	HQRTHTGEKPYKCPECGK		
E3	GEKPYKCPECGKSFS	SDCRDLAR	HQRTHTGEKPYKCPECGK		
	170	180			
E2C	SFSRSDKLVR	HQRTHTGKKTSGQAG		SEQ ID NO: 125	
E3	SFSQSSHLVR	HQRTHTGKKTSGQAG		SEQ ID NO: 126	

Fig. 2